Amendments to the Specification:

Insert the paper copy of the Sequence Listing filed herewith following the Drawings.

Please amend the paragraph beginning at page 15, line 31, as follows:

Figs. 3A-3C: Specific elements required for *skn-1*-independent and -dependent GCS-1::GFP expression. 3A: Analysis of the *gcs-1* promoter. Expression of the indicated constructs from transgenic extrachromosomal arrays was assayed in 2-3 independent transgenic lines, under normal conditions and after induction by paraquat and heat. Approximate relative expression levels in the tissues designated to the right (data not shown) are indicated by + signs, with ++ indicating a reproducible reduction, and ++ indicating barely detectable expression. Within each set of transgenic lines that carried promoter mutations, levels of normal and induced expression were affected in parallel. Mutations that were created in predicted SKN-1 sites 1, 2, and 3 are described in Materials and Methods, and are not compatible with SKN-1 binding (see text). Red ovals indicate predicted SKN-1 binding sites and a green bar the 5' end of the *gcs-1::gfp* coding region. Map numbers refer to the predicted translation start. 3B: Uncoupling pharyngeal GCS-1::GFP expression from intestinal and ASI neuron expression. The *gcsΔ 2* mutation eliminated pharyngeal GCS-1::GFP expression, but allowed near-wild type levels of ASI and intestinal expression. Concurrent ablation of SKN-1 binding site 3 (*gcsΔ 2,mut3*) eliminated transgene expression in all tissues. Paraquat-treated worms are shown in the GFP column. 3C: Composite *gcs-1* promoter element that includes SKN-1 site 3 (SEQ ID NO:55), and is also present in the *med-1* and *-2* promoters (SEQ ID NO:56) and (SEQ ID NO:57). SKN-1 binding sites are red, and identical sequences are boxed.

Please amend the paragraph beginning at page 17, line 31, as follows:

Fig. 7 illustrates an exemplary regulatory sequence (SEQ ID NO:18) for the glutathione synthetase gene.

Please amend the paragraph beginning at page 17, line 33, as follows:

Fig. 8 illustrates the sequences of the glutathione synthetase ORF (SEQ ID NO:19) and protein (SEQ ID NO:20).

Please amend the paragraph beginning at page 17, line 33, as follows:

Fig. 9 illustrates an exemplary regulatory sequence (SEQ ID NO:21) for the NADH quinone oxidoreductase gene.

Please amend the paragraph beginning at page 18, line 5, as follows:

Fig. 10 illustrates the sequences of the NADH quinone oxidoreductase ORF (SEQ ID NO:22) and protein (SEQ ID NO:23).

Please amend the paragraph beginning at page 18, line 7, as follows:

Fig. 11 illustrates an exemplary regulatory sequence (SEQ ID NO:24) for the glutathione S-transferase (R03D7.6) gene.

Please amend the paragraph beginning at page 18, line 9, as follows:

Fig. 12 illustrates the sequences of the glutathione S-transferase (R03D7.6) ORF (SEQ ID NO:25) and protein (SEQ ID NO:26).

Please amend the paragraph beginning at page 18, line 11, as follows:

Fig. 13 illustrates an exemplary regulatory sequence (SEQ ID NO:27) for the glutathione S-transferase (F35E8.8) gene.

Please amend the paragraph beginning at page 18, line 13, as follows:

Fig. 14 illustrates the sequences of the glutathione S-transferase (F35E8.8) ORF (SEQ ID NO:28) and protein (SEQ ID NO:29).

Please amend the paragraph beginning at page 18, line 15, as follows:

Fig. 15 illustrates an exemplary regulatory sequence (SEQ ID NO:30) for the glutathione S-transferase (F11G11.2) gene.

Please amend the paragraph beginning at page 18, line 17, as follows:

Fig. 16 illustrates the sequences of the glutathione S-transferase (F11G11.2) ORF (SEQ ID NO:31) and protein (SEQ ID NO:32).

Please amend the paragraph beginning at page 18, line 19, as follows:

Fig. 17 illustrates an exemplary regulatory sequence (SEQ ID NO:33) for the glutathione S-transferase (K08F4.7) gene.

Please amend the paragraph beginning at page 18, line 21, as follows:

Fig. 18 illustrates the sequences of the glutathione S-transferase (K08F4.7) ORF (SEQ ID NO:34) and protein (SEQ ID NO:35).

Please amend the paragraph beginning at page 18, line 23, as follows:

Fig. 19 illustrates an exemplary regulatory sequence (SEQ ID NO:36) for the superoxide dismutase-1 (*sod-1*) gene.

Please amend the paragraph beginning at page 18, line 25, as follows:

Fig. 20 illustrates the sequences of the superoxide dismutase-1 (*sod-1*) ORF (SEQ ID NO:37) and protein (SEQ ID NO:38).

Please amend the paragraph beginning at page 18, line 27, as follows:

Fig. 21 illustrates an exemplary regulatory sequence (SEQ ID NO:39) for the superoxide dismutase-2 (*sod-2)* gene.

Please amend the paragraph beginning at page 18, line 29, as follows:

Fig. 22 illustrates the sequences of the superoxide dismutase-2 (*sod-2)* ORF (SEQ ID NO:40) and protein (SEQ ID NO:41).

Please amend the paragraph beginning at page 18, line 31, as follows:

Fig. 23 illustrates an exemplary regulatory sequence (SEQ ID NO:42) for the catalase (*ctl-1)* gene.

Please amend the paragraph beginning at page 18, line 33, as follows:

Fig. 24 illustrates the sequences of the catalase (*ctl-1)* ORF (SEQ ID NO:43) and protein (SEQ ID NO:44).

Please amend the paragraph beginning at page 18, line 34, as follows:

Fig. 25 illustrates an exemplary regulatory sequence (SEQ ID NO:45) for the superoxide dismutase-3 (*sod-3)* gene.

Please amend the paragraph beginning at page 19, line 5, as follows:

Fig. 26 illustrates the sequences of the superoxide dismutase-3 (*sod-3)* ORF (SEQ ID NO:46) and protein (SEQ ID NO:47).

Please amend the paragraph beginning at page 19, line 7, as follows:

Fig. 27 illustrates an exemplary regulatory sequence (SEQ ID NO:48) for the γ-glutamine cysteine synthase (also known as glutamate-cysteine ligase) heavy chain gene.

Please amend the paragraph beginning at page 19, line 9, as follows:

Fig. 28 illustrates the sequences of the γ-glutamine cysteine synthase (also known as glutamate-cysteine ligase) heavy chain open reading frame (ORF) (SEQ ID NO:49) and protein (SEQ ID NO:50).

Please amend the paragraph beginning at page 19, line 12, as follows:

Fig. 29 illustrates the sequences of the T19E7.2c SKN-1 (SEQ ID NO:4), ORF (SEQ ID NO:3) and protein (SEQ ID NO:2).

Please amend the paragraph beginning at page 19, line 13, as follows:

Fig. 30 illustrates the sequences of the T19E7.2b SKN-1 (SEQ ID NO:8), ORF (SEQ ID NO:6) and protein (SEQ ID NO:7).

Please amend the paragraph beginning at page 19, line 14, as follows:

Fig. 31 illustrates the sequences of the T19E7.2a SKN-1 (SEQ ID NO:12), ORF (SEQ ID NO:9) and protein (SEQ ID NO:10).

Please amend the paragraph beginning at page 19, line 15, as follows:

Fig. 32 illustrates the amino acid sequence (SEQ ID NO:13) of human GSK-3 beta.

Please amend the paragraph beginning at page 19, line 16, as follows:

Fig. 33 illustrates the amino acid sequence (SEQ ID NO:14) of human GSK-3 alpha.

Please amend the paragraph beginning at page 19, line 17, as follows:

Fig. 34 illustrates the amino acid sequence (SEQ ID NO:15) of mouse GSK-3 beta.

Please amend the paragraph beginning at page 19, line 18, as follows:

Fig. 35 illustrates the amino acid sequence (SEQ ID NO:16) of mouse GSK-3 alpha.

Please amend the paragraph beginning at page 19, line 19, as follows:

Fig. 36 illustrates the amino acid sequence (SEQ ID NO:17) of *C. elegans* GSK-3.

Please amend the paragraph beginning at page 19, line 24, as follows:

Fig. 39 is (A) a schematic of predicted phosphorylation sites (SEQ ID NO:51), (SEQ ID NO:52), (SEQ ID NO:53) and (SEQ ID NO:54) and (B) a graph of phosphorylation of various SKN-1 peptides by GSK-3.

Please amend the paragraph beginning at page 20, line 14, as follows:

The *C. elegans* genome has been sequenced (see, e.g., The *C. elegans* Sequencing Consortium, Science 282, p.2012-2018, 1998), and is accessible through several known electronic databases (see, e.g., the databases accessible at World Wide Web (www) addresses: wormbase.org (WormBase; see, Harris et al., Nucleic Acids Research 31:133-137 (2003), and Stein et al., Nucleic Acids Research 29:82-86 (2001)); ncbi.nlm.nih.gov; and wormbase.sanger.ac.uk). "SKN-1 DNA" or "SKN-1 gene" refers to nucleic acid sequences that include, e.g., the nucleic sequence set forth in Fig. 29 (or the unspliced version thereof) (set forth in the WormBase database as T19E7.2c) and/or Fig. 31 or 30 (or the unspliced versions thereof) (set forth in the WormBase database as T19E7.2a, and T19E7.2b, respectively), homologs thereof, or fragments thereof that encodes SKN-1 polypeptide fragment capable of binding a SKN-1 protein binding site within a promoter of a target gene, e.g., a *C. elegans* Phase II detoxification gene. An example of such a fragment is a fragment that encodes the C-terminal 85 amino acid residues (SEQ ID NO:1) of the SKN-1 polypeptide set forth in Fig. 29 (referred to herein as a "SKN-1 Domain"). By "SKN-1 polypeptide" is meant an amino acid sequence that includes an amino acid sequence set forth in Figs. 29, 30 and/or 31, or fragments thereof (e.g., the C-terminal 85 amino acid residues (SEQ ID NO:1) of the SKN-1 polypeptide set forth in Fig. 29 (a "SKN-1 Domain), or amino acids 381-403 (SEQ ID NO:5) set forth in Fig. 29, or amino acids 473-495 (SEQ ID NO:11) set forth in Fig. 31). By "SKN-1 RNA" is meant messenger RNA transcribed from a SKN-1 DNA sequence.